

Technical Product Report

For Research Use Only; Not for use in Diagnostic Procedures

Product Description: Seraseq® ctDNA Mutation Mix v2 WT

Material No: 0710-0144 Batch Number: 10396366

Material Description: Human genomic DNA from the reference cell line, GM24385.

Date of Manufacture: 19-Feb-2019 Expiration Date: 19-Feb-2021

Concentration (Qubit dsDNA BR Assay): 14.9 ng/μL

Volume: 25 μL

Storage: -20 °C

Digital PCR testing
using BioRad
QX200™ Droplet
Digital™ PCR
System:

Gene ID	COSMIC Identifier	AF% ¹
AKT1	COSM33765	0.03
APC	COSM13127	0.05
APC	COSM18561	0.00
ATM	COSM21924	0.00
BRAF	COSM476	0.00
CTNNB1	COSM5664	0.02
EGFR	COSM6224	0.02
EGFR	COSM12378	0.02
EGFR	COSM6225	0.00
EGFR	COSM6240	0.02
ERBB2	COSM682/20959	0.00
FGFR3	COSM715	0.00
FLT3	COSM783	0.00
FOXL2	COSM33661	0.00
GNA11	COSM52969	0.00
GNAQ	COSM28758	0.00
GNAS	COSM27887	0.06
IDH1	COSM28747	0.08
JAK2	COSM12600	0.00
KIT	COSM1314	0.01
KRAS	COSM521	0.02
MPL	COSM18918	0.00
NCOA4-RET	N/A	0.00
NPM1	COSM17559	0.00
NRAS/CSDE1	COSM584	0.09
PDGFRA	COSM736	0.03
PDGFRA	COSM28053	0.00
PIK3CA	COSM763	0.03
PIK3CA	COSM12464	0.00
PIK3CA	COSM775	0.10
PTEN	COSM4986	0.00
PTEN	COSM5809	0.00
RET	COSM965	0.01
SMAD4	COSM14105	0.01
TP53	COSM10648	0.05
TP53	COSM10660	0.03
TP53	COSM10662	0.07
TP53	COSM6530	0.00
TP53	COSM18610	Not Tested ²
TPR-ALK	N/A	0.01

¹ Variant allele frequencies > 0.00% for this wildtype negative control are within the expected range for stochastic positive dPCR reactions.

² NGS testing alone is used for QC of variant COSM18610.

NGS was performed as an orthogonal verification step. Results confirm no variants were detected above 0.1%, except for the TP53 COSM10648 and TP53 COSM10662 variants which were detected at 0.1% in the WT sample; the corresponding dPCR data was 0.05% and 0.07% respectively. Thus, we associate the allele frequency for both TP53 COSM10648 and TP53 COSM10662 variants with the background from the assay¹ using the conditions listed below.

NGS Parameters:

DNA input = 50 ng

of samples / flow cell = 2

of total reads / sample = 8.4 M

Average read depth = 9000X

On-target reads = ~92.7 %

Q30 score = ~93 %

Analysis = Archer Analysis Suite v5.1.7; Default analysis settings except for the following:

- ERROR_CORRECTION is turned to ON (default=OFF; cfDNA pipeline)
- MAPQ_THRESHOLD_FOR_VARIANT_CALL is set to 10 (default=0)
- MIN_ALLELE_FRACTION_FOR_VARIANT_CALL is set to 0.00025 (default=0.001)
- MIN_BASEQUAL_FOR_VARIANT_CALL is set to 30 (default=20)
- NORMALIZATION_LEVEL is set to 10000000 (default is 3500000; cfDNA pipeline)
- VARIANT_DOWNSTREAM_ROI_SIZE is set to 150 (default=400; cfDNA pipeline)

¹Please see the poster from NIST for more information about assay sensitivity:

<https://digital.seracare.com/multilab-assessment-reference-materials-ctdna-poster2018>

Next Generation Sequencing testing using Archer® Reveal ctDNA™ 28 Kit run on an Illumina® MiSeq™ using v2 (2x150 bp) PE chemistry reagents:

Approval:



Prepared By

26-Feb-2019

Date